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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2008; month=4; day=15; hr=18; min=27; sec=10; ms=270;]

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Application No: 09866379 Version No: 1.0

Input Set:

Output Set:

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Finished: 2008-04-15 17:58:49.639
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 628 ms
Total Warnings: 4
Total Errors: 0
No. of SeqIDs Defined: 10
Actual SeqID Count: 10

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
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W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)

SEQUENCE LISTING

<110> Short, Jay M.
 Kretz, Keith A.
 Gray, Kevin A.
 Barton, Nelson Robert
 Garrett, James B.
 O' Donoghue, Eileen
 Mathur, Eric J.

<120> RECOMBINANT BACTERIAL PHYTASES AND USES
 THEREOF

<130> 564462001822

<140> 09866379

<141> 2001-05-24

<150> US 09/580,515

<151> 2000-05-25

<150> US 09/318,528

<151> 1999-05-25

<150> US 09/291,931

<151> 1999-04-13

<150> US 09/259,214

<151> 1999-03-01

<150> US 08/910,798

<151> 1997-08-13

<160> 10

<170> FastSEQ for Windows Version 4.0

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<211> 1323

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1320)

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<222> 216

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5

10

15

ccg caa tct gca ttc gct cag agt gag ccg gag ctg aag ctg gaa agt	96
Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser	
20 25 30	
gtg gtg att gtc agt cgt cat ggt gtg cgt gct cca acc aag gcc acg	144
Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr	
35 40 45	
caa ctg atg cag gat gtc acc cca gac gca tgg cca acc tgg ccg gta	192
Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val	
50 55 60	
aaa ctg ggt tgg ctg aca ccg cgn ggt ggt gag cta atc gcc tat ctc	240
Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu	
65 70 75 80	
gga cat tac caa cgc cag cgt ctg gta gcc gac gga ttg ctg gcg aaa	288
Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Ala Lys	
85 90 95	
aag ggc tgc ccg cag tct ggt cag gtc gcg att att gct gat gtc gac	336
Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp	
100 105 110	
gag cgt acc cgt aaa aca ggc gaa gcc ttc gcc gcc ggg ctg gca cct	384
Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro	
115 120 125	
gac tgt gca ata acc gta cat acc cag gca gat acg tcc agt ccc gat	432
Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp	
130 135 140	
ccg tta ttt aat cct cta aaa act ggc gtt tgc caa ctg gat aac gcg	480
Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala	
145 150 155 160	
aac gtg act gac gcg atc ctc agc agg gca gga ggg tca att gct gac	528
Asn Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile Ala Asp	
165 170 175	
ttt acc ggg cat cgg caa acg gcg ttt cgc gaa ctg gaa cgg gtg ctt	576
Phe Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu	
180 185 190	
aat ttt ccg caa tca aac ttg tgc ctt aaa cgt gag aaa cag gac gaa	624
Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu	
195 200 205	
agc tgt tca tta acg cag gca tta cca tcg gaa ctc aag gtg agc gcc	672
Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala	
210 215 220	
gac aat gtc tca tta acc ggt gcg gta agc ctc gca tca atg ctg acg	720
Asp Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr	
225 230 235 240	
gag ata ttt ctc ctg caa caa gca cag gga atg ccg gag ccg ggg tgg	768

Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp	
245	250 255
gga agg atc acc gat tca cac cag tgg aac acc ttg cta agt ttg cat	816
Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His	
260	265 270
aac gcg caa ttt tat ttg cta caa cgc acg cca gag gtt gcc cgc agc	864
Asn Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser	
275	280 285
cgc gcc acc ccg tta ttg gat ttg atc atg gca gcg ttg acg ccc cat	912
Arg Ala Thr Pro Leu Leu Asp Leu Ile Met Ala Ala Leu Thr Pro His	
290	295 300
cca ccg caa aaa cag gcg tat ggt gtg aca tta ccc act tca gta ctg	960
Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu	
305	310 315 320
ttt att gcc gga cac gat act aat ctg gca aat ctc ggc ggc gca ctg	1008
Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu	
325	330 335
gag ctc aac tgg acg ctt ccc ggt cag ccg gat aac acg ccg cca ggt	1056
Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly	
340	345 350
ggg gaa ctg gtg ttt gaa cgc tgg cgt cgg cta agc gat aac agc cag	1104
Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln	
355	360 365
tgg att cag gtt tcg ctg gtc ttc cag act tta cag cag atg cgt gat	1152
Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp	
370	375 380
aaa acg ccg ctg tca tta aat acg ccg ccc gga gag gtg aaa ctg acc	1200
Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr	
385	390 395 400
ctg gca gga tgt gaa gag cga aat gcg cag ggc atg tgt tcg ttg gca	1248
Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala	
405	410 415
ggg ttt acg caa atc gtg aat gaa gca cgc ata ccg gcg tgc agt ttg	1296
Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu	
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aga tct cat cac cat cac cat cac taa	1323
Arg Ser His His His His His His	
435	440

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<211> 440

<212> PRT

<213> Escherichia coli

<400> 2

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20 25 30
Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr
35 40 45
Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val
50 55 60
Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu
65 70 75 80
Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Ala Lys
85 90 95
Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp
100 105 110
Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro
115 120 125
Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp
130 135 140
Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala
145 150 155 160
Asn Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile Ala Asp
165 170 175
Phe Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu
180 185 190
Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu
195 200 205
Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala
210 215 220
Asp Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr
225 230 235 240
Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp
245 250 255
Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His
260 265 270
Asn Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser
275 280 285
Arg Ala Thr Pro Leu Leu Asp Leu Ile Met Ala Ala Leu Thr Pro His
290 295 300
Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu
305 310 315 320
Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu
325 330 335
Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly
340 345 350
Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln
355 360 365
Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp
370 375 380
Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr
385 390 395 400
Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala
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420 425 430
Arg Ser His His His His His His
435 440

<210> 3
 <211> 49
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

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 <210> 4
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 4
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 <210> 5
 <211> 1901
 <212> DNA
 <213> Escherichia coli

 <220>
 <221> misc_feature
 <222> 403
 <223> n = A,T,C or G

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 tgatgcggcg cattagcatc gcatcaggca atcaataatg tcagatatga aaagcggaaa 180
 catatcgatg aaagcgatct taatcccatt tttatctctt ctgattccgt taaccccgca 240
 atctgcattc gctcagagtg agccggagct gaagctggaa agtgtggtga ttgtcagtcg 300
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 gctgacggag atattttctc tgcaacaagc acagggaatg ccggagccgg ggtggggaag 960
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 gacagcgttg acgccccatc caccgcaaaa acaggcgtat ggtgtgacat taccacttct 1140
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cattcagtta	cctgaatgct	ctgaggctga	tgacaaacga	agaactgtct	aatgcgtaga	1560
ccggaanaag	cgttcacgcc	gcacccggcc	actttcagtt	ttcctctttc	tcggagtaac	1620
tataaccgta	atagttatag	ccgtaactgt	aagcgggtgt	ggcgcgttta	atcacaccat	1680
tgaggatagc	gcctttaata	ttgacgcctg	cctgttccag	acgctgcatt	gacaaaactca	1740
cctctttggc	ggtgttcaag	ccaaaacgcg	caaccagcag	gctggtgcca	acagaacgcc	1800
ccacgaccgc	ggcatcactc	accgccagca	tcggcggcgt	atcgacaata	accagatcgt	1860
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<211> 1901

<212> DNA

<213> Escherichia coli

<220>

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<223> n = A,T,C or G

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tgatgcggcg	cattagcatc	gcacagggca	atcaataatg	tcagatatga	aaagcggaaa	180
catatcgatg	aaagcgatct	taatcccat	tttatctctt	ctgattccgt	taaccgccga	240
atctgcattc	gctcagagtg	agccggagct	gaagctggaa	agtgtggtga	ttgtcagtcg	300
tcattggtgtg	cgtgctccaa	ccaaggccac	gcaactgatg	caggatgtca	ccccagacgc	360
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ctatctcgga	cattacctgg	gccagcgtct	ggtagccgac	ggattgctgg	cgaaaaaggg	480
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agatacgtcc	agtcccgatc	cgttatttta	tcctctaaaa	actggcggtt	gccaaactgga	660
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ggaactcaag	gtgagcgccg	acaatgtctc	attaaccggt	gcggttaagc	tcgcatcaat	900
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gatcaccgat	tcacaccagt	ggaacacctt	gctaagtttg	cataacgcgc	aattttattt	1020
gctacaacgc	acgccagagg	ttgcccgag	ccgcgccacc	ccgttattag	atttgatcaa	1080
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caactggacg	cttcccggtc	agccggataa	cacgcgcgca	ggtggtgaac	tggtgtttga	1260
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tataaccgta	atagttatag	ccgtaactgt	aagcgggtgt	ggcgcgttta	atcacaccat	1680
tgaggatagc	gcctttaata	ttgacgcctg	cctgttccag	acgctgcatt	gacaaaactca	1740
cctctttggc	ggtgttcaag	ccaaaacgcg	caaccagcag	gctggtgcca	acagaacgcc	1800
ccacgaccgc	ggcatcactc	accgccagca	tcggcggcgt	atcgacaata	accagatcgt	1860
aatggtcggt	cgcccatctc	agtaattgac	gcacccgata	g		1901

<210> 7

<211> 1901

<212> DNA

<213> Escherichia coli

<220>

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<222> (188)...(1483)

<221> misc_feature

<222> 403

<223> n = A,T,C or G

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tgatgcggcg cattagcatc gcacaggca atcaataatg tcagatatga aaagcggaaa	180
catatcg atg aaa gcg atc tta atc cca ttt tta tct ctt ctg att ccg	229

Met	Lys	Ala	Ile	Leu	Ile	Pro	Phe	Leu	Ser	Leu	Leu	Ile	Pro
1				5								10	

tta acc ccg caa tct gca ttc gct cag agt gag ccg gag ctg aag ctg	277		
Leu Thr Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu			
15	20	25	30

gaa agt gtg gtg att gtc agt cgt cat ggt gtg cgt gct cca acc aag	325	
Glu Ser Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys		
35	40	45

gcc acg caa ctg atg cag gat gtc acc cca gac gca tgg cca acc tgg	373	
Ala Thr Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp		
50	55	60

ccg gta aaa ctg ggt tgg ctg aca ccg cgn ggt ggt gag cta atc gcc	421	
Pro Val Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala		
65	70	75

tat ctc gga cat tac caa cgc cag cgt ctg gta gcc gac gga ttg ctg	469	
Tyr Leu Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu		
80	85	90

gcg aaa aag ggc tgc ccg cag tct ggt cag gtc gcg att att gct gat	517		
Ala Lys Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp			
95	100	105	110

gtc gac gag cgt acc cgt aaa aca ggc gaa gcc ttc gcc gcc ggg ctg	565	
Val Asp Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu		
115	120	125

gca cct gac tgt gca ata acc gta cat acc cag gca gat acg tcc agt	613	
Ala Pro Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser		
130	135	140

ccc gat ccg tta ttt aat cct cta aaa act ggc gtt tgc caa ctg gat	661	
Pro Asp Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp		
145	150	155

aac gcg aac gtg act gac gcg atc ctc agc agg gca gga ggg tca att	709	
Asn Ala Asn Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile		
160	165	170

gct gac ttt acc ggg cat cgg caa acg gcg ttt cgc gaa ctg gaa cgg	757
Ala Asp Phe Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg	
175 180 185 190	
gtg ctt aat ttt ccg caa tca aac ttg tgc ctt aaa cgt gag aaa cag	805
Val Leu As	